

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: June, Carl H.  
Thompson, Craig B.  
Nabel, Gary J.  
Gray, Gary S.  
Rennert, Paul D.

(ii) TITLE OF INVENTION: Methods For Selectively Stimulating  
Proliferation Of T-Cells

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD  
(B) STREET: 60 State Street, Suite 510  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.  
(B) REGISTRATION NUMBER: 36,207  
(C) REFERENCE/DOCKET NUMBER: RPI-002CP2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400  
(B) TELEFAX: (617) 227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1491 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapien

(F) TISSUE TYPE: lymphoid

(G) CELL TYPE: B cell

(H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA in pCDM8 vector

(B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

(A) NAME/KEY: Open reading frame (translated region)

(B) LOCATION: 318 to 1181 bp

(C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

(A) NAME/KEY: Alternate polyadenylation signal

(B) LOCATION: 1474 to 1479 bp

(C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

(A) AUTHORS: FREEMAN, GORDON J.

FREEDMAN, ARNOLD S.

SEGIL, JEFFREY M.

LEE, GRACE

WHITMAN, JAMES F.

NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With  
Unique Expression On Activated And Neoplastic B Cells

(C) JOURNAL: The Journal of Immunology

(D) VOLUME: 143

(E) ISSUE: 8

(F) PAGES: 2714-2722

(G) DATE: 15-OCT-1989

(H) RELEVANT RESIDUES In SEQ ID NO:1: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60

09350202-070899

	GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT	120
5	GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT	180
	GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT	240
	TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGGGCTTT CACTTTTGAC	300
10	CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC	353
	Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser	
	-30 -25	
15	AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT	401
	Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu	
	-20 -15 -10	
20	TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA	449
	Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu	
	-5 1 5 10	
25	GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA	497
	Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala	
	15 20 25	
30	CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG	545
	Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met	
	30 35 40	
35	ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC	593
	Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile	
	45 50 55	
40	TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA	641
	Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro	
	60 65 70	
45	TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC	689
	Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp	
	75 80 85 90	
50	GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT	737
	Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala	
	95 100 105	
55	GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT	785
	Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn	
	110 115 120	

5	ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His 125 130 135	833
10	CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr 140 145 150	881
15	GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu 155 160 165 170	929
20	GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr 175 180 185	977
25	GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln 190 195 200	1025
30	GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile 205 210 215	1073
35	TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala 220 225 230	1121
40	CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser 235 240 245 250	1169
45	GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA Val Arg Pro Val	1221
50	GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT	1281 1341
55	AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC	1401 1461

AATTCATTAT CTATTAAACA CTAATTTGAG

1491

5 (3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 288 amino acids  
(B) TYPE: amino acid-  
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 15 (A) DESCRIPTION: B cell activation antigen; natural ligand  
for CD28 T cell surface antigen; transmembrane protein

(ix) FEATURE:

- 20 (A) NAME/KEY: signal sequence  
(B) LOCATION: -34 to -1  
(C) IDENTIFICATION METHOD: amino terminal sequencing of  
soluble protein  
25 (D) OTHER INFORMATION: hydrophobic

(ix) FEATURE:

- 30 (A) NAME/KEY: extracellular domain  
(B) LOCATION: 1 to 208  
(C) IDENTIFICATION METHOD: similarity with known  
sequence

(ix) FEATURE:

- 35 (A) NAME/KEY: transmembrane domain  
(B) LOCATION: 209 to 235  
(C) IDENTIFICATION METHOD: similarity with known  
sequence  
40

(ix) FEATURE:

- 45 (A) NAME/KEY: intracellular domain  
(B) LOCATION: 236 to 254  
(C) IDENTIFICATION METHOD: similarity with known  
sequence

50 (ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 19 to 21  
55 (C) IDENTIFICATION METHOD: similarity with known  
sequence

00350202 070899 568020 2020560

(ix) FEATURE:

- 5 (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 55 to 57  
(C) IDENTIFICATION METHOD: similarity with known sequence

10 (ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 64 to 66  
(C) IDENTIFICATION METHOD: similarity with known sequence

15 (ix) FEATURE:

- 20 (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 152 to 154  
(C) IDENTIFICATION METHOD: similarity with known sequence

25 (ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 173 to 175  
(C) IDENTIFICATION METHOD: similarity with known sequence

30 (ix) FEATURE:

- 35 (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 177 to 179  
(C) IDENTIFICATION METHOD: similarity with known sequence

40 (ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 192 to 194  
(C) IDENTIFICATION METHOD: similarity with known sequence

45 (ix) FEATURE:

- 50 (A) NAME/KEY: N-linked glycosylation  
(B) LOCATION: 198 to 200  
(C) IDENTIFICATION METHOD: similarity with known sequence

55 (ix) FEATURE:

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668020"2020560

- (A) NAME/KEY: Ig V-set domain  
 (B) LOCATION: 1 to 104  
 (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain  
 (B) LOCATION: 105 to 202  
 (C) IDENTIFICATION METHOD: similarity with known sequence

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.  
 FREEDMAN, ARNOLD S.  
 SEGIL, JEFFREY M.  
 LEE, GRACE  
 WHITMAN, JAMES F.  
 NADLER, LEE M.  
 (B) TITLE: B7, A New Member Of The Ig Superfamily With  
 Unique Expression On Activated And Neoplastic B Cells  
 (C) JOURNAL: The Journal of Immunology  
 (D) VOLUME: 143  
 (E) ISSUE: 8  
 (F) PAGES: 2714-2722  
 (G) DATE: 15-OCT-1989  
 (H) RELEVANT RESIDUES IN SEQUENCE ID NO:2: From -26 to 262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr  
 -30 -25 -20  
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys  
 -15 -10 -5  
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu  
 -1 1 5 10  
 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile  
 15 20 25 30  
 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp  
 35 40 45  
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr  
 50 55 60  
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly  
 65 70 75

00350200 00000000

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg  
80 85 90

5 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr  
95 100 105 110

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile  
115 120 125

10 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu  
130 135 140

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp  
145 150 155

15 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met  
160 165 170

20 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg  
175 180 185 190

25 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro  
195 200 205

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly  
210 215 220

30 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg  
225 230 235

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val  
240 245 250

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT



	GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
	Met Asp Pro	
	1	
5	CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
	Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
	5 10 15	
10	CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
	Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
	20 25 30 35	
15	GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
	Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
	40 45 50	
20	GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
	Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
	55 60 65	
25	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
	Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
	70 75 80	
30	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
	Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
	85 90 95	
35	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
	Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
	100 105 110 115	
40	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
	Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
	120 125 130	
45	GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
	Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
	135 140 145	
50	ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
	Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
	150 155 160	
55	CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
	Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
	165 170 175	
60	ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
	Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
	180 185 190 195	
65	CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
	Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	
	200 205 210	

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AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT 787  
Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu  
215 220 225

5 TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA 835  
Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro  
230 235 240

10 GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT 883  
Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys  
245 250 255

15 GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG 931  
Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg  
260 265 270 275

20 CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG 979  
Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu  
280 285 290

AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT 1027  
Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser  
295 300 305

25 GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC 1075  
Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp  
310 315 320

30 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA 1120  
Lys Ser Asp Thr Cys Phe  
325

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

45 Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met  
1 5 10 15

Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe  
20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln  
35 40 45

55 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val  
50 55 60

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Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser  
65 70 75 80

5 Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg  
85 90 95

Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile  
100 105 110

10 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser  
115 120 125

Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile  
130 135 140

15 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile  
145 150 155 160

20 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys  
165 170 175

Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn  
180 185 190

25 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro  
195 200 205

30 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys  
210 215 220

Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln  
225 230 235 240

35 Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val  
245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys  
260 265 270

40 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu  
275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro  
290 295 300

45 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser  
305 310 315 320

50 Ser Cys Asp Lys Ser Asp Thr Cys Phe  
325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids

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(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Gln Phe Cys Asp His Trp Gly Cys Trp Leu Leu Arg Glu Thr His  
5 10 15  
Ile Phe Thr Pro  
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Arg Leu Val Leu Glu Asp Pro Gly Ile Trp Leu Arg Pro Asp Tyr  
5 10 15  
Phe Phe Pro Ala  
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Cys Trp Leu Leu Arg Glu  
5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10

Gly Ile Trp Leu Arg Pro Asp  
5

15 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /label=Xaa is Asp or Glu

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Xaa Gly Xaa Trp Leu Xaa Xaa Xaa Xaa  
5

35

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

50 TO BE REPLACED

(2) INFORMATION FOR SEQ ID NO:11:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

10 Gly Leu Trp Leu Arg Phe Asp  
5

15 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Xaa Trp Leu Xaa Xaa  
5

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